

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: WUCHERPFENNIG, Kai W
STROMINGER, Jack L
- (ii) TITLE OF INVENTION: MONOVALENT, MULTIVALENT AND MULTIMERIC MHC
BINDING DOMAIN FUSION PROTEINS AND ONJUGATES, AND USES THEREFOR
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: TESTA, HURWITZ & THIBEAULT, LLP
(B) STREET: 125 HIGH STREET
(C) CITY: BOSTON
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02110
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/024,077
(B) FILING DATE: 16-AUG-1996
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/US97/14503
(B) FILING DATE: 15-AUG-1997
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 60/075,351
(B) FILING DATE: 19-FEB-1998
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Twomey, Michael J
(B) REGISTRATION NUMBER: 38,349
(C) REFERENCE/DOCKET NUMBER: HAR-005
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (617) 248 7000
(B) TELEFAX: (617) 248 7100

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 750 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..735

- (ix) FEATURE:

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(A) NAME/KEY: misc feature
 (B) LOCATION: 1..21
 (D) OTHER INFORMATION: /note= "3' end of secretory signal"

(ix) FEATURE:

(A) NAME/KEY: misc feature
 (B) LOCATION: 22..594
 (D) OTHER INFORMATION: /note= "DRA*0101 extracellular domain"

(ix) FEATURE:

(A) NAME/KEY: misc feature
 (B) LOCATION: 595..7615
 (D) OTHER INFORMATION: /note= "Linker sequence"

(ix) FEATURE:

(A) NAME/KEY: misc feature
 (B) LOCATION: 616..735
 (D) OTHER INFORMATION: /note= "Fos leucine zipper domain"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTA	TCT	CTC	GAG	AAA	AGA	GAG	ATC	AAA	GAA	GAA	CAT	GTG	ATC	ATC	CAG	48
Val	Ser	Leu	Glu	Lys	Arg	Glu	Ile	Lys	Glu	Glu	His	Val	Ile	Ile	Gln	
1				5				10						15		
GCC	GAG	TTC	TAT	CTG	AAT	CCT	GAC	CAA	TCA	GGC	GAG	TTT	ATG	TTT	GAC	96
Ala	Glu	Phe	Tyr	Leu	Asn	Pro	Asp	Gln	Ser	Gly	Glu	Phe	Met	Phe	Asp	
			20					25					30			
TTT	GAT	GGT	GAT	GAG	ATT	TTC	CAT	GTG	GAT	ATG	GCA	AAG	AAG	GAG	ACG	144
Phe	Asp	Gly	Asp	Glu	Ile	Phe	His	Val	Asp	Met	Ala	Lys	Lys	Glu	Thr	
		35				40						45				
GTC	TGG	CGG	CTT	GAA	GAA	TTT	GGA	CGA	TTT	GCC	AGC	TTT	GAG	GCT	CAA	192
Val	Trp	Arg	Leu	Glu	Glu	Phe	Gly	Arg	Phe	Ala	Ser	Phe	Glu	Ala	Gln	
	50					55				60						
GGT	GCA	TTG	GCC	AAC	ATA	GCT	GTG	GAC	AAA	GCC	AAC	TTG	GAA	ATC	ATG	240
Gly	Ala	Leu	Ala	Asn	Ile	Ala	Val	Asp	Lys	Ala	Asn	Leu	Glu	Ile	Met	
65				70					75					80		
ACA	AAG	CGC	TCC	AAC	TAT	ACT	CCG	ATC	ACC	AAT	GTA	CCT	CCA	GAG	GTA	288
Thr	Lys	Arg	Ser	Asn	Tyr	Thr	Pro	Ile	Thr	Asn	Val	Pro	Pro	Glu	Val	
				85					90					95		
ACT	GTG	CTC	ACG	AAC	AGC	CCT	GTG	GAA	CTG	AGA	GAG	CCC	AAC	GTC	CTC	336
Thr	Val	Leu	Thr	Asn	Ser	Pro	Val	Glu	Leu	Arg	Glu	Pro	Asn	Val	Leu	
			100					105					110			
ATC	TGT	TTC	ATA	GAC	AAG	TTC	ACC	CCA	CCA	GTG	GTC	AAT	GTC	ACG	TGG	384
Ile	Cys	Phe	Ile	Asp	Lys	Phe	Thr	Pro	Pro	Val	Val	Asn	Val	Thr	Trp	
		115				120						125				
CTT	CGA	AAT	GGA	AAA	CCT	GTC	ACC	ACA	GGA	GTG	TCA	GAG	ACA	GTC	TTC	432
Leu	Arg	Asn	Gly	Lys	Pro	Val	Thr	Thr	Gly	Val	Ser	Glu	Thr	Val	Phe	
		130				135					140					
CTG	CCC	AGG	GAA	GAC	CAC	CTT	TTC	CGC	AAG	TTC	CAC	TAT	CTC	CCC	TTC	480
Leu	Pro	Arg	Glu	Asp	His	Leu	Phe	Arg	Lys	Phe	His	Tyr	Leu	Pro	Phe	
145					150					155				160		
CTG	CCC	TCA	ACT	GAG	GAC	GTT	TAC	GAC	TGC	AGG	GTG	GAG	CAC	TGG	GGC	528
Leu	Pro	Ser	Thr	Glu	Asp	Val	Tyr	Asp	Cys	Arg	Val	Glu	His	Trp	Gly	
				165				170						175		
TTG	GAT	GAG	CCT	CTT	CTC	AAG	CAC	TGG	GAG	TTT	GAT	GCT	CCA	AGC	CCT	576
Leu	Asp	Glu	Pro	Leu	Leu	Lys	His	Trp	Glu	Phe	Asp	Ala	Pro	Ser	Pro	

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Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser Ala Leu
 210 215 220
 Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe
 225 230 235 240
 Ile Leu Ala Ala His
 245

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..756

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "3' end of secretory signal"

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 22..615
- (D) OTHER INFORMATION: /note= "DRB1*1501 extracellular domain"

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 616..736
- (D) OTHER INFORMATION: /note= "Linker sequence"

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 637..756
- (D) OTHER INFORMATION: /note= "Jun leucine zipper domain"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTA TCT CTC GAG AAA AGA GAG GGG GAC ACC CGA CCA CGT TTC CTG TGG	48
Val Ser Leu Glu Lys Arg Glu Gly Asp Thr Arg Pro Arg Phe Leu Trp	
1 5 10 15	
CAG CCT AAG AGG GAG TGT CAT TTC TTC AAT GGG ACG GAG CGG GTG CGG	96
Gln Pro Lys Arg Glu Cys His Phe Phe Asn Gly Thr Glu Arg Val Arg	
20 25 30	
TTC CTG GAC AGA TAC TTC TAT AAC CAG GAG GAG TCC GTG CGC TTC GAC	144
Phe Leu Asp Arg Tyr Phe Tyr Asn Gln Glu Glu Ser Val Arg Phe Asp	
35 40 45	
AGC GAC GTG GGG GAG TTC CGG GCG GTG ACG GAG CTG GGG CGG CCT GAC	192
Ser Asp Val Gly Glu Phe Arg Ala Val Thr Glu Leu Gly Arg Pro Asp	
50 55 60	
GCT GAG TAC TGG AAC AGC CAG AAG GAC ATC CTG GAG CAG GCG CGG GCC	240
Ala Glu Tyr Trp Asn Ser Gln Lys Asp Ile Leu Glu Gln Ala Arg Ala	
65 70 75 80	
GCG GTG GAC ACC TAC TGC AGA CAC AAC TAC GGG GTT GTG GAG AGC TTC	288
Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly Val Val Glu Ser Phe	

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85										90					95					
ACA	GTG	CAG	CGG	CGA	GTC	CAA	CCT	AAG	GTG	ACT	GTA	TAT	CCT	TCA	AAG	336				
Thr	Val	Gln	Arg	Arg	Val	Gln	Pro	Lys	Val	Thr	Val	Tyr	Pro	Ser	Lys					
			100					105					110							
ACC	CAG	CCC	CTG	CAG	CAC	CAC	AAC	CTC	CTG	GTC	TGC	TCT	GTG	AGT	GGT	384				
Thr	Gln	Pro	Leu	Gln	His	His	Asn	Leu	Leu	Val	Cys	Ser	Val	Ser	Gly					
		115					120					125								
TTC	TAT	CCA	GGC	AGC	ATT	GAA	GTC	AGG	TGG	TTC	CTG	AAC	GGC	CAG	GAA	432				
Phe	Tyr	Pro	Gly	Ser	Ile	Glu	Val	Arg	Trp	Phe	Leu	Asn	Gly	Gln	Glu					
	130					135					140									
GAG	AAG	GCT	GGG	ATG	GTG	TCC	ACA	GGC	CTG	ATC	CAG	AAT	GGA	GAC	TGG	480				
Glu	Lys	Ala	Gly	Met	Val	Ser	Thr	Gly	Leu	Ile	Gln	Asn	Gly	Asp	Trp					
145					150				155						160					
ACC	TTC	CAG	ACC	CTG	GTG	ATG	CTG	GAA	ACA	GTT	CCT	CGA	AGT	GGA	GAG	528				
Thr	Phe	Gln	Thr	Leu	Val	Met	Leu	Glu	Thr	Val	Pro	Arg	Ser	Gly	Glu					
			165						170					175						
GTT	TAC	ACC	TGC	CAA	GTG	GAG	CAC	CCA	AGC	GTG	ACA	AGC	CCT	CTC	ACA	576				
Val	Tyr	Thr	Cys	Gln	Val	Glu	His	Pro	Ser	Val	Thr	Ser	Pro	Leu	Thr					
		180						185					190							
GTG	GAA	TGG	AGA	GCA	CGG	TCT	GAA	TCT	GCA	CAG	AGC	AAG	GTC	GAC	GGA	624				
Val	Glu	Trp	Arg	Ala	Arg	Ser	Glu	Ser	Ala	Gln	Ser	Lys	Val	Asp	Gly					
		195					200					205								
GGT	GGC	GGC	GGT	CGC	ATC	GCC	CGG	CTC	GAG	GAA	AAA	GTG	AAA	ACC	TTG	672				
Gly	Gly	Gly	Gly	Arg	Ile	Ala	Arg	Leu	Glu	Glu	Lys	Val	Lys	Thr	Leu					
	210					215					220									
AAA	GCT	CAG	AAC	TCG	GAG	CTC	GCG	TCC	ACG	GCC	AAC	ATG	CTC	AGG	GAA	720				
Lys	Ala	Gln	Asn	Ser	Glu	Leu	Ala	Ser	Thr	Ala	Asn	Met	Leu	Arg	Glu					
225					230					235					240					
CAG	GTG	GCA	CAG	CTT	AAA	CAG	AAA	GTC	ATG	AAC	CAT	TGAGAATTCT				766				
Gln	Val	Ala	Gln	Leu	Lys	Gln	Lys	Val	Met	Asn	His									
			245					250												
ATGAC																771				

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Val	Ser	Leu	Glu	Lys	Arg	Glu	Gly	Asp	Thr	Arg	Pro	Arg	Phe	Leu	Trp
1				5					10					15	
Gln	Pro	Lys	Arg	Glu	Cys	His	Phe	Phe	Asn	Gly	Thr	Glu	Arg	Val	Arg
			20					25					30		
Phe	Leu	Asp	Arg	Tyr	Phe	Tyr	Asn	Gln	Glu	Glu	Ser	Val	Arg	Phe	Asp
		35					40					45			
Ser	Asp	Val	Gly	Glu	Phe	Arg	Ala	Val	Thr	Glu	Leu	Gly	Arg	Pro	Asp
	50					55					60				
Ala	Glu	Tyr	Trp	Asn	Ser	Gln	Lys	Asp	Ile	Leu	Glu	Gln	Ala	Arg	Ala

09248964-024299

-81-

65 70 75 80
 Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly Val Val Glu Ser Phe
 85 90 95
 Thr Val Gln Arg Arg Val Gln Pro Lys Val Thr Val Tyr Pro Ser Lys
 100 105 110
 Thr Gln Pro Leu Gln His His Asn Leu Leu Val Cys Ser Val Ser Gly
 115 120 125
 Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp Phe Leu Asn Gly Gln Glu
 130 135 140
 Glu Lys Ala Gly Met Val Ser Thr Gly Leu Ile Gln Asn Gly Asp Trp
 145 150 155 160
 Thr Phe Gln Thr Leu Val Met Leu Glu Thr Val Pro Arg Ser Gly Glu
 165 170 175
 Val Tyr Thr Cys Gln Val Glu His Pro Ser Val Thr Ser Pro Leu Thr
 180 185 190
 Val Glu Trp Arg Ala Arg Ser Glu Ser Ala Gln Ser Lys Val Asp Gly
 195 200 205
 Gly Gly Gly Gly Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu
 210 215 220
 Lys Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu
 225 230 235 240
 Gln Val Ala Gln Leu Lys Gln Lys Val Met Asn His
 245 250

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: misc feature
 (B) LOCATION: 1..42
 (D) OTHER INFORMATION: /note= "synthetic, PCR primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTATCTCTCG AGAAAAGAGA GATCAAAGAA GAACATGTGA TC

42

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: misc feature
 (B) LOCATION: 1..39
 (D) OTHER INFORMATION: /note= "synthetic, PCR primer"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
GTCATAGAAT TCTCAATGGG CGGCCAGGAT GAACTCCAG 39

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: misc feature
(B) LOCATION: 1..42
(D) OTHER INFORMATION: /note= "synthetic, PCR primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
GTATCTCTCG AGAAAAGAGA GGGGGACACC CGACCACGTT TC 42

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: misc feature
(B) LOCATION: 1..39
(D) OTHER INFORMATION: /note= "synthetic, PCR primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
GTCATAGAAT TCTCAATGGT TCATGACTTT CTGTTTAAG 39

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: misc feature
(B) LOCATION: 1..14
(D) OTHER INFORMATION: /note= "synthetic, biotin ligase recognition sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Leu Gly Gly Ile Phe Glu Ala Met Lys Met Glu Leu Arg Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:10:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION: 1..16
 (D) OTHER INFORMATION: /note= "synthetic, linker sequence"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ser Gly Gly Gly Ser Leu Val Pro Arg Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

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